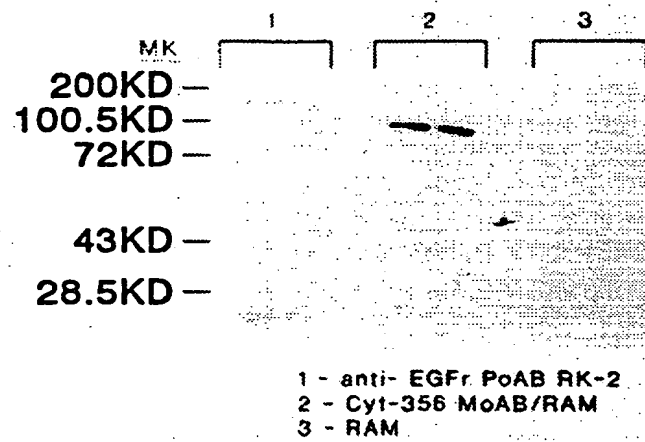


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FIGURE 1



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FIGURE 2A

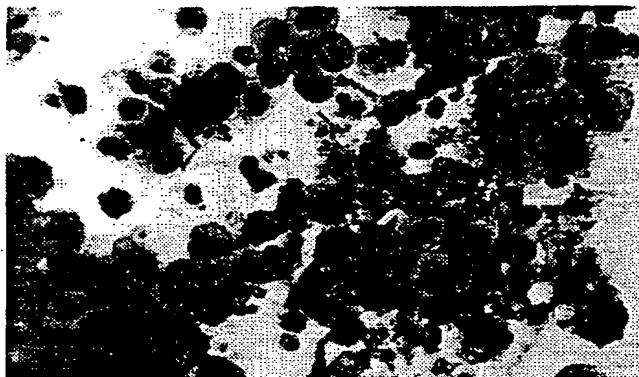


FIGURE 2B

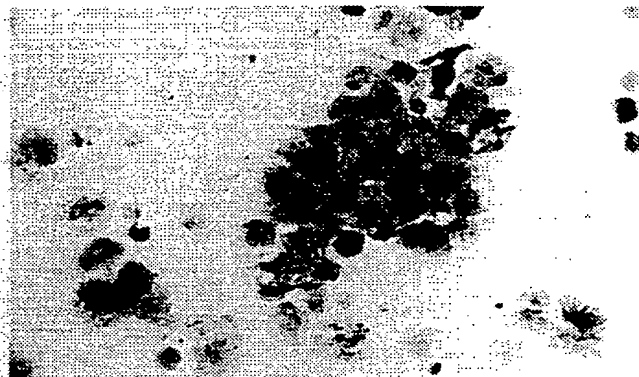


FIGURE 2C

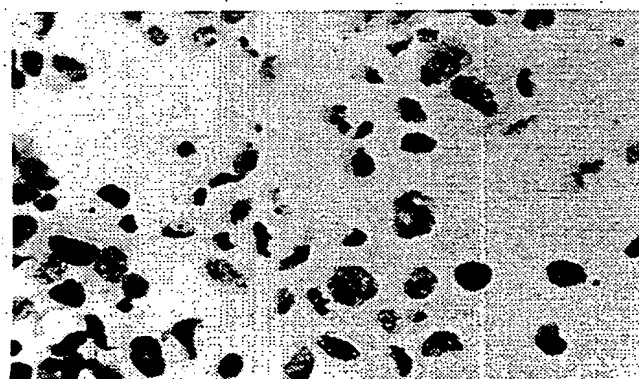
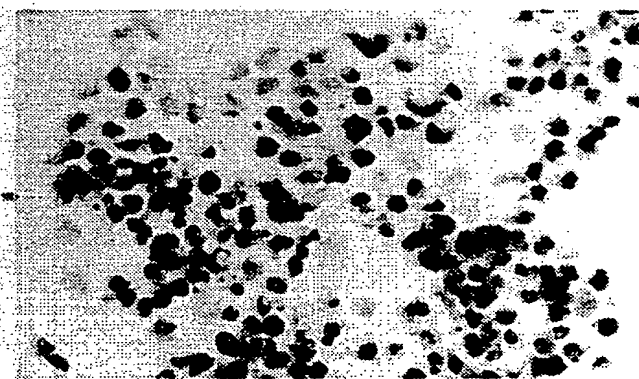


FIGURE 2D



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FIGURE 3A

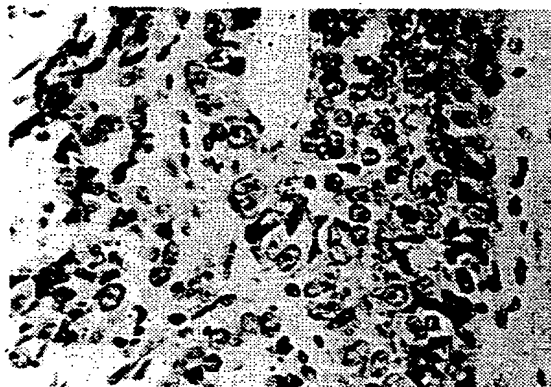


FIGURE 3B

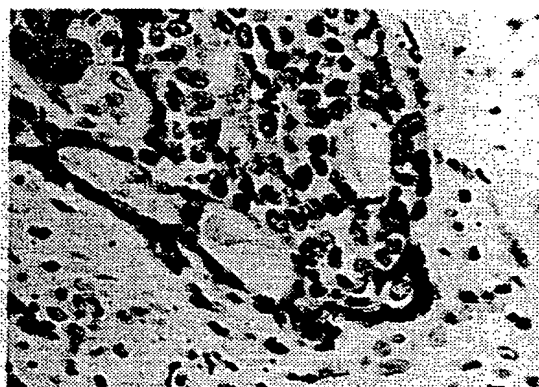


FIGURE 3C

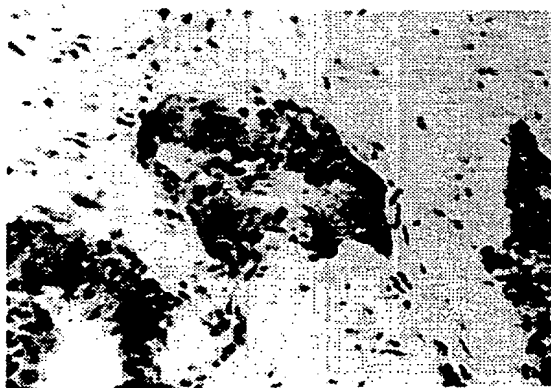
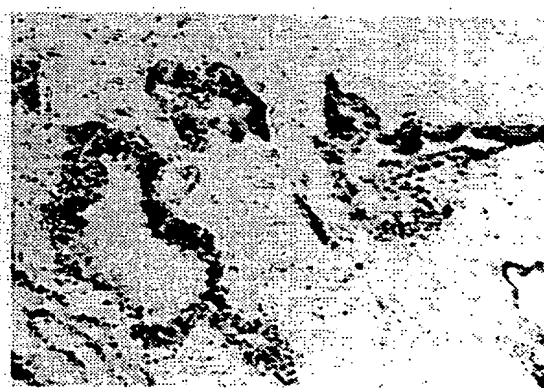
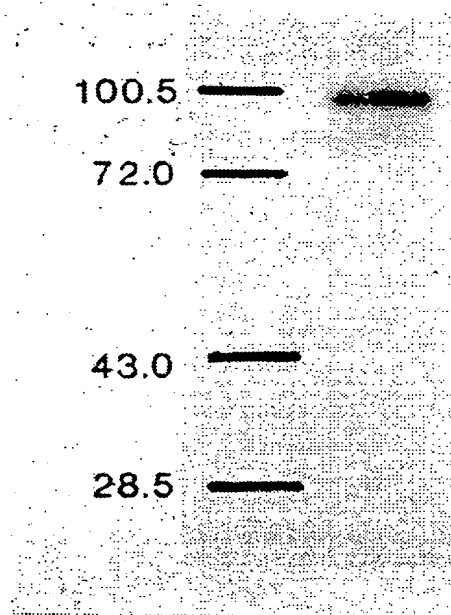


FIGURE 3D



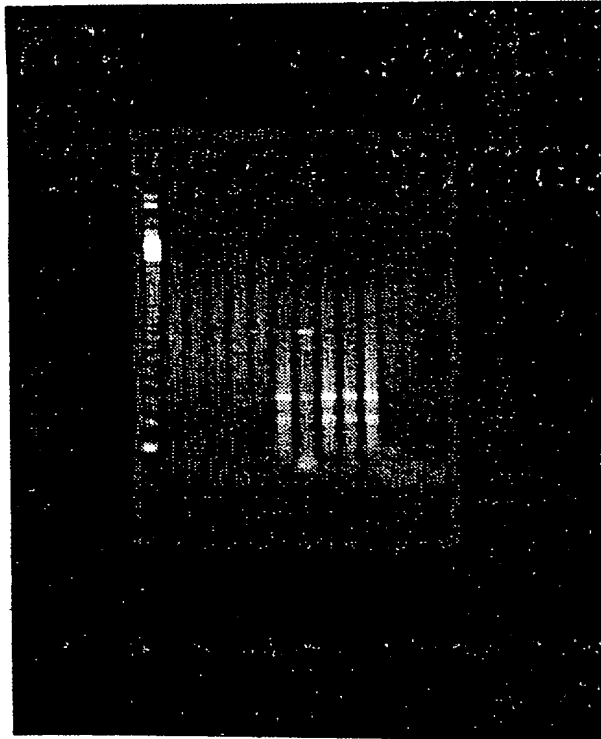
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FIGURE 4



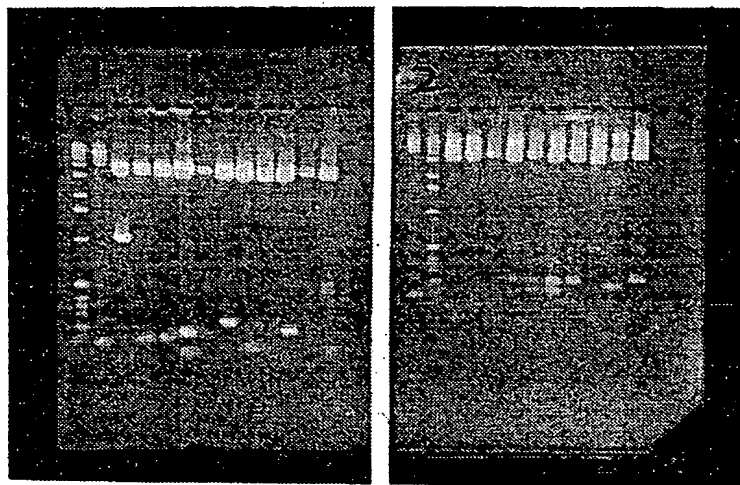
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FIGURE 5



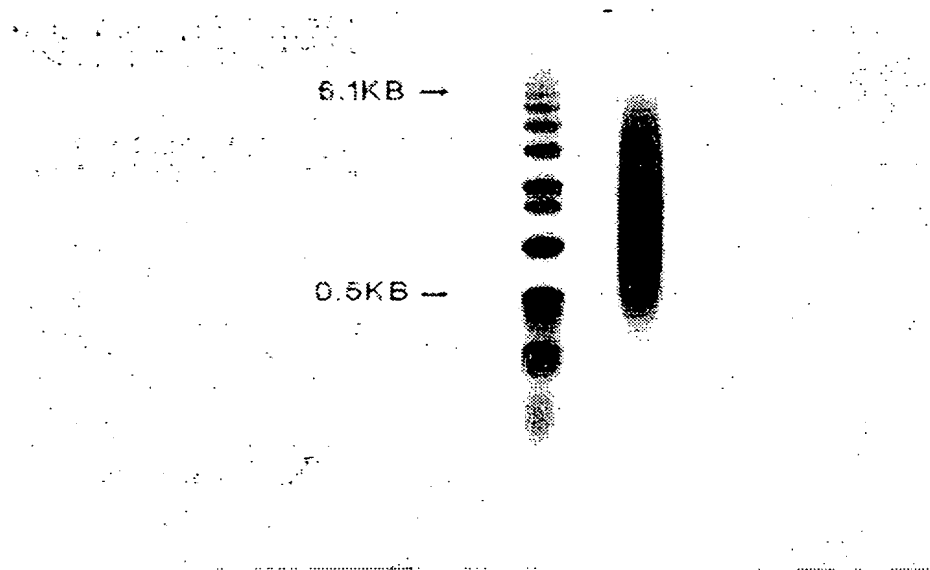
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FIGURE 6A FIGURE 6B



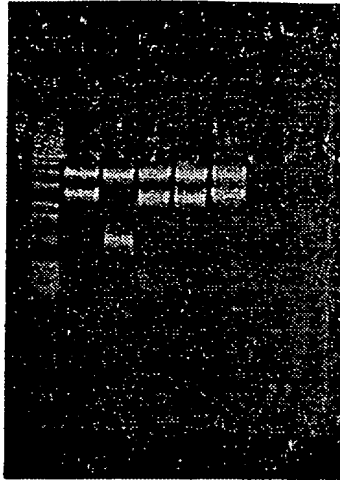
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FIGURE 7



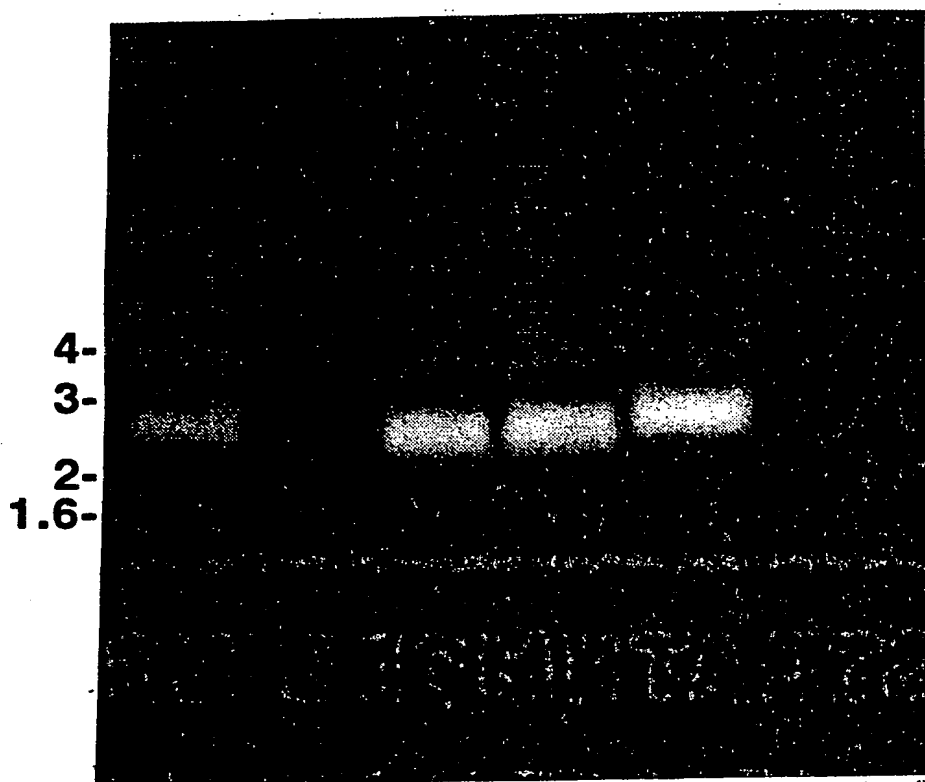
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FIGURE 8



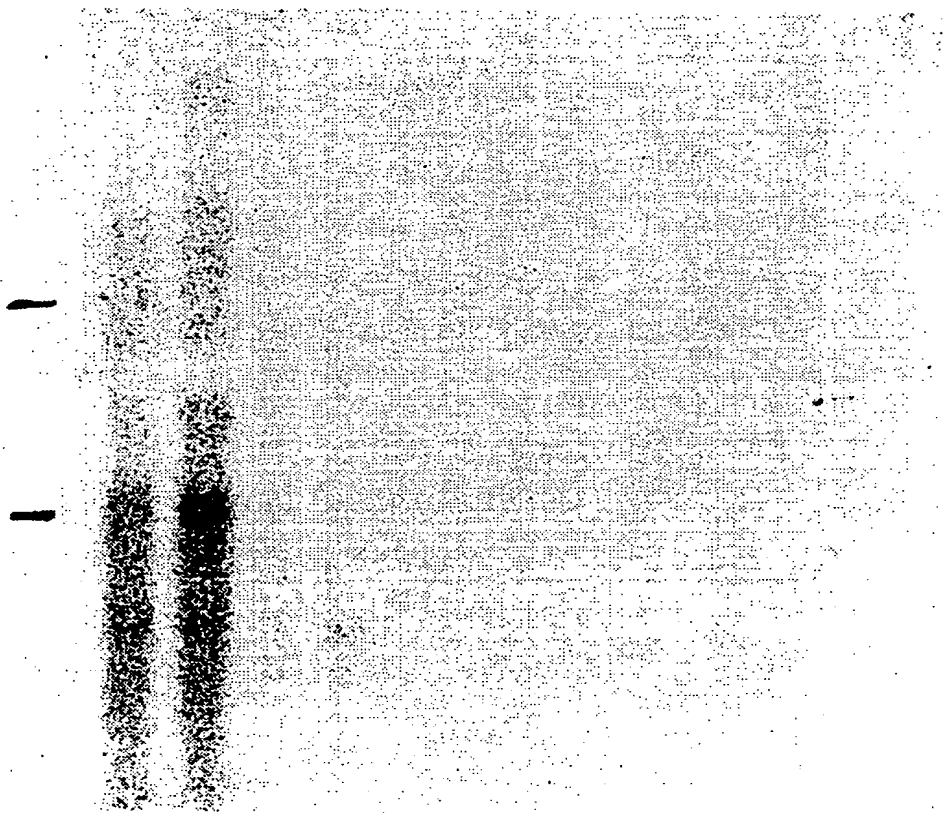
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FIGURE 9



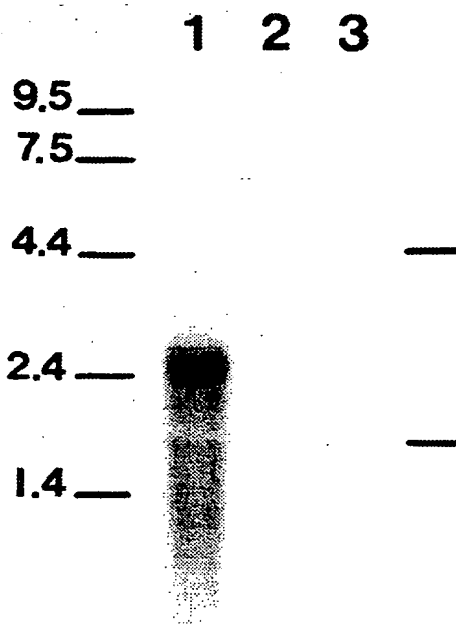
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FIGURE 10



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FIGURE 11



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FIGURE 12A

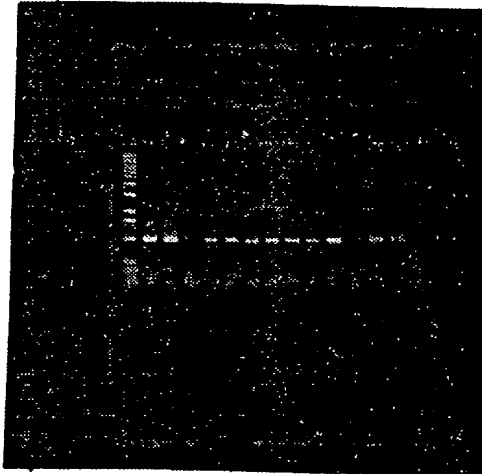
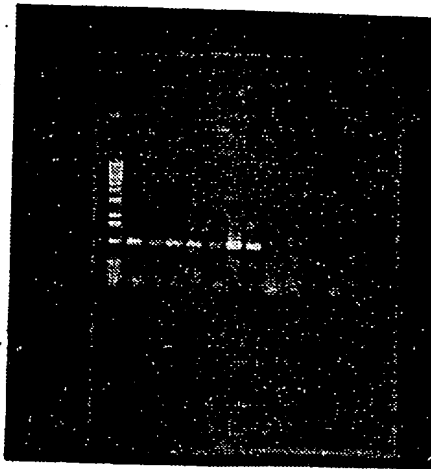
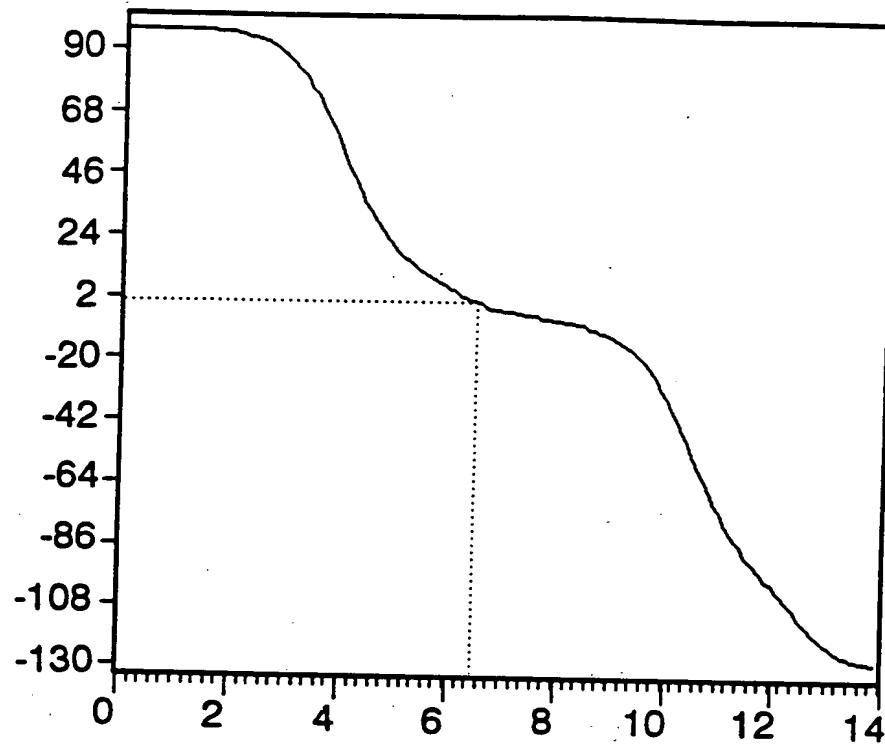


FIGURE 12B



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FIGURE 13



Analysis done on the complete sequence.

In Helical	(H)	conformation	[DC =	-75	CNAT]	:	264	AA	=>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT]	:	309	AA	=>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT]	:	76	AA	=>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT]	:	101	AA	=>	13.4%

Sequence shown with conformation codes.

Consecutive stretch of 5 or more residues in a given conformation are overlined.

[illegible]

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FIGURE 14-2

91	H	H	H	H	E	H	C	E	E	E	T	T	C	S	H	H	H	H	H	H	H	E	E	E	E	E	E	T
121	T	T	C	S	E	E	E	E	E	E	E	C	T	C	S	H	E	E	E	E	E	T	T	C	C	C	T	T
151	T	E	E	E	E	E	E	E	E	E	E	E	T	E	C	C	T	C	C	E	E	E	E	E	E	E	E	H
181	H	H	H	H	H	H	H	H	H	H	H	H	H	H	T	T	T	E	E	E	E	E	E	E	E	E	E	E
211	T	T	C	S	H	H	H	H	H	H	H	E	E	E	E	E	E	E	T	E	E	E	E	E	E	E	E	E
241	E	E	T	T	T	E	C	S	T	T	C	E	E	E	E	E	E	E	E	E	T	T	C	E	E	E	E	E
271	C	C	S	E	E	E	E	H	E	E	E	E	E	E	E	E	E	C	E	E	E	E	E	E	E	E	E	E
301	H	H	H	H	H	H	E	T	T	C	C	C	T	E	T	T	E	T	E	T	E	E	E	E	E	E	E	E
331	E	E	E	C	E	H	H	H	H	H	E	E	C	C	C	C	E	E	E	E	E	E	E	E	E	E	E	E
361	E	E	E	E	E	E	E	E	E	E	E	E	E	C	C	C	T	E	E	E	E	T	C	C	C	T	C	C
391	C	H	H	E	E	E	H	H	H	H	H	H	C	C	C	T	T	C	C	C	T	E	E	E	E	E	E	C
421	H	H	H	H	H	H	H	C	C	C	S	H	H	H	H	H	H	H	H	H	H	E	E	E	E	E	E	E
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

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FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNLLHETDS	AVATARRPRWLCAGALVLAGGFFLLGLFGWFIKSSNEAT			
XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX
XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX
60	70	80	90	100
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW				


```

>----->--**>--**>-----XXXXXXXXXXXXXXXXXX>>--
>----->--**>--**>-----XXXXXXXXXXXXXXXXXX>>--
210      220      230      240      250
|         |         |         |         |
VIARYGVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG
----->>--**XXXXXXXX-->----->>-->>-->>--**>
----->>--**XXXXXXXX-->----->>-->>-->>--**>
260      270      280      290      300
|         |         |         |         |
GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYV
>*----->>>--*-----**>-----XX-->-----**>-----
>*----->>>--*-----**>-----XX-->-----**>-----
310      320      330      340      350
|         |         |         |         |
DAQLLEKMGSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHISTN
XXXXXXXXX->>>--**>-->>-->-----*--XXXXXXXX-->-----*--*--*--*--
XXXXXXXXX->>>--**>-->>-->-----*--XXXXXXXX-->-----*--*--*--*--
360      370      380      390      400
|         |         |         |         |
EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR

```

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FIGURE 14-7

```

-----
-----
SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQERGVAI
410      420      430      440      450
|         |         |         |         |
XXX***>>>***>-----***>----->***>***XXX-----XX
XXX***>>>***>-----***>----->***>***XXX-----XX
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKK
460      470      480      490      500
|         |         |         |         |
----->>-----XXX*-----XXX*-----XXX*----->>*
----->>-----XXX*-----XXX*-----XXX*----->>*
SPSPEFGMPRISKLGSGNDFEVFQRLGIASGRARYTKNWETNKFSGYP
510      520      530      540      550
|         |         |         |         |
***>----->***>-----XXX*----->>----->>***>
***>----->***>-----XXX*----->>----->>***>
560      570      580      590      600
|         |         |         |         |

```

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FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXX-X-----XXXXX----->XXX
 -----XXXXXXXXXXXXX-X-----XXXXX----->XXX

610 620 630 640 650
 | | | | |
 AVVLRKYADKIYSISMKHPQEMKTVSVSFDLSFAVKNFTEIASKFSERL

XXXXXXXXXX-----X**XXXXX-----XXXXXXXXXXXXXXXXXXXX
 XXXXXXXXXXXX-----X**XXXXX-----XXXXXXXXXXXXXXXXXXXX

660 670 680 690 700
 | | | | |
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY

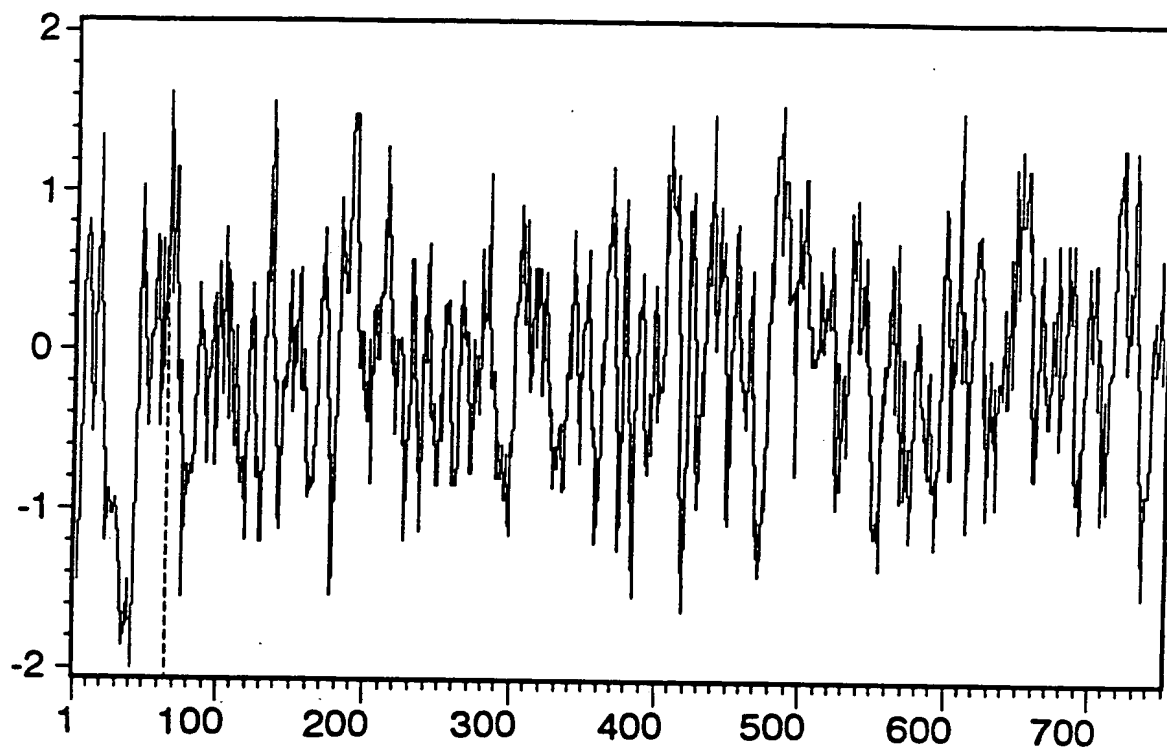
XX>>>***-----XXXXXXXXXX-->>***>----->***>
 XX>>>***-----XXXXXXXXXX-->>***>----->***>

710 720 730 740 750
 | | | | |
 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAETLSEVA

----->--XXXXXXXXXX***XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX
 ----->--XXXXXXXXXX***XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX

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FIGURE 15A



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FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

 The three highest points of hydrophilicity are:

(1)	Ah= 1.62	: From	63 to	68	: Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah= 1.57	: From	132 to	137	: Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah= 1.55	: From	482 to	487	: Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

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FIGURE 16-2

```
1200      1210      1220      1230      1240      1250
pmsgen AGCACCAACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CACATGCTCTGA-AG--GTTGGAAAGGTGCGGATCCA---TTCCTGTAAGGT--GAC--AA
1170      1180      1190      1200      1210

1260      1270      1280      1290      1300      1310
pmsgen CTTTACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAAAGCAGGAGA----GCCAGA-TAATGGTGAAACTAGATGTGAACAATTCCCATGAAAGA
1220      1230      1240      1250      1260

1320      1330      1340      1350      1360      1370
pmsgen GACAAGAAATTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAACAGACAGATATGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAGGAAGATTCTGAACATCTTCGGTGCTATCCAGGGATTGGAAGAACCTGATCGGTATGT
1270      1280      1290      1300      1310      1320

1380      1390      1400      1410      1420      1430
pmsgen CATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TGTGATTGAGCCAGAGAGACTCCTGGGGCCAGGAGTGGCTAAAGCTGGCAGCTGGAAC
1330      1340      1350      1360      1370      1380
```

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	1620	1630	1640	1650	1660	1670
pmsgen	TGC-TGACTCATCTATAGAAAGGAACATA-CACTCTGAGAGTTGATTGTACACCGCTGATG					
	:: :: : :: :	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :
CHKTFE	-GCTTGGATGCTCCAGTCCTGGGAGCAAGCCATGTCAAGATTTCCTGCCAGCCCCCTTGCTG					
	1570	1580	1590	1600	1610	1620

	1680	1690	1700	1710	1720	1730
pmsgen	TACAGCTGGTACACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGC					
	::: :::	:	::: :::	::: :::	::: :::	::: :::
CHKTFE	TATATGCTGGGAGTATTATGAAGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC					
	1630	1640	1650	1660	1670	1680

```

1740      1750      1760      1770      1780      1790
pmsgen  AAATCTCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCC
          :::: :: :: :::: :: ::
CHKTFE  ----CTCTATAACAGACTTGGCCCAGACTGGGTAAAGCAGTTGTTCCTCTTGGCCCTGGA
          1690      1700      1710      1720      1730

```

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```

1260      1270      1280      1290      1300      1310
pmsgen  -TACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----
          :  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
RATTRF  CTCATGTAAGCTGGAACTTTCACAGAAATCAAAATGTGAAGCTCACTGTGAACAAATGTACT
670      680      690      700      710      720

```

pmmsen --AAGTGACAAGAA TTTACAAATGTGATAGTACTCTCAGAGGAGCAGTGGAACCAGACAG
RATTRF GAAAGAAAACAAGAATACTTAACATCTTTGGCGTTATTAAAGGCTATGAGGAACCAGACCG

730 740 750 760 770 780

1380 1390 1400 1410 1420 1430
pmsgen ATATGTCATTCTGGAGGTCACCGGACTCATGGTGTTGGTGATTTGACCCCTCAGAG
:: : : :::: : : : : : : : : : : : : : : : :
RATTRF CTACATTGTAGGAGCCCGAGAGACGCTTGGGGCCCTGGT-GTTGCCGAAGTCCAGTG
790 800 810 820 830 840

pmngen T-GGAGCAGCTGTGTTTCATGAATAATTGTGAGGAGCTTGGAAACA-CTGA---AAAAGCAA
:
RATTRF TGGGAACAGGTCTT-CTGTTGAAACTTGCCCCAAGTATTCTCAGATATGATTTCAAAAGAT

1440	1450	1460	1470	1480
850	860	870	880	890
900				

[illegible]

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	1610	1620	1630	1640	1650	1660
pmsgen	GCTTATATAATGCTGACTCATCTATAGAAAGAACTA-CAC	CTGAGAGTTGATTGTAC				
	:::: :::::: :::	:	:	:::: :::	:	:
RATTRF	ACTTACATTAAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG					
	1030	1040	1050	1060	1070	1080

```

1670      1680      1690      1700      1710      1720
pmsgen  ACCGCTGATGACAGCTTGGTACACAACCTAACAAAGAGCTGAAAGC-CCTGATGAAG
        :: :: : :: : : : : : : : : : : : : : : : : : : : :
RATTRF  CCCCCTATTATATACACTTATGGGGAAGATAATGCCAGGA--CGTAAAGCATCCGA-----
1090      1100      1110      1120      1130

```

FIGURE 16-8

```

1730      1740      1750      1760      1770
pmsgen GCTTGAAGGCAAACTCTCTTAT-GAA-----AGTTGGACTAAAAAAGTCCTTCCCCCAG
      : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : :
RATTRF ---TTGATGGAAAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
      1140      1150      1160      1170      1180      1190
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1780      1790      1800      1810      1820      1830
pmsgen AGTTCAGTGGCATGCCCAGGATAAGCAAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT
      1200      1210      1220      1230      1240      1250
RATTRF CCTTGGACAATGCTGCATTCCTTTTCTTGCAATTCAGGAATCCCAGCAGTTTCTTTCT

```

FIGURE 16-9

HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266
54.3% identity in 464 nt overlap

```

1230      1240      1250      1260      1270
pmsgen AGAAGTCTCAAAGTGCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC
          : : : : : : : : : : : : : : : : : :
HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAACAGACTCTACATGTAGGATGGTAACCTC
1140      1150      1160      1170      1180      1190

```

```

1280      1290      1300      1310      1320      1330
pmsgen AAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
          : : : : : : : : : : : : : : : : : :
HUMTFR AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA
1200      1210      1220      1230      1240      1250

```

```

1340      1350      1360      1370      1380      1390
pmsgen TGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAAGACAGATATGTCATCTCTGGGAGGTCA
          : : : : : : : : : : : : : : : : : :
HUMTFR CATCTTTGGAGTTAATAAGGCTTTGTAGAACCAAGATCACTATGTTGTAGTTGGGGCCCA
1260      1270      1280      1290      1300      1310

```

```

1400      1410      1420      1430      1440      1450
pmsgen CCGGGACTCATGGGTGTTTGGTGTATTGACCCCTCAGAGT-GGAGCAGCTGTTGTTTCATG
          : : : : : : : : : : : : : : : : : :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
1320      1330      1340      1350      1360      1370

```

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pmsgen AAATTG---TGAGGAGCTTTGGAAACACTGAAAAGGAAGGTGGAGACCTAGAAGAACAA
:: :: :: :: :: :: :: :: :: X :: :: :: :: :: :: ::
HUMTFR AACTTGCCCAAGATGTTCTCAGATATGGTCTTAAAAAGATGGGTTTCAGCCCAGCAGAAGCA
1380 1390 1400 1410 1420 1430

	1510	1520	1530	1540	1550	1560
pmsgen	TTTTGTTTGC	AAGCTGGATG	CAGAAGAA	TTCGTCTT	GCTTCTACT	GAGTGGCAG
	:: : :::::	:: : :::	:: : :::	:: : :::	:: : :::	:: : :::
HUMTFR	TTATCTTTGCC	AGTTGGAGTG	CTGGAGACTT	TGGATCGG	TGGTGCCAC	TGAATGGCTAG
	1440	1450	1460	1470	1480	1490

[illegible]

1630 1640 1650 1660 1670 1680
 pmsgen ATAGAAGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC
 : : : : : : : : : : : :
 HUNTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACGCTTATTGAG
 1560 1570 1580 1590 1600 1610

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FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAA	TCTCTTATG			
:	:	:	:	:	:
HUMTER	AAAACAATGC AAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

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FIGURE 17A

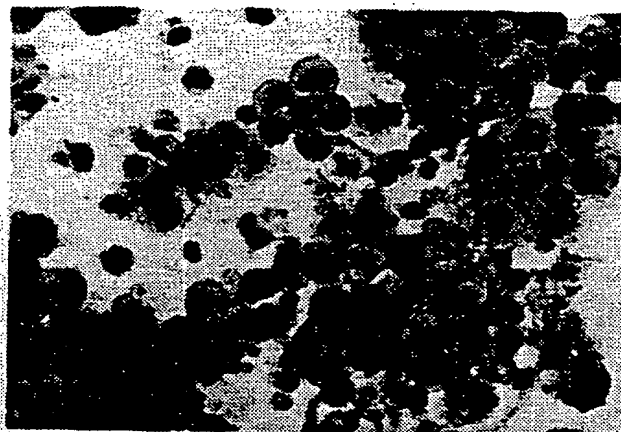


FIGURE 17B

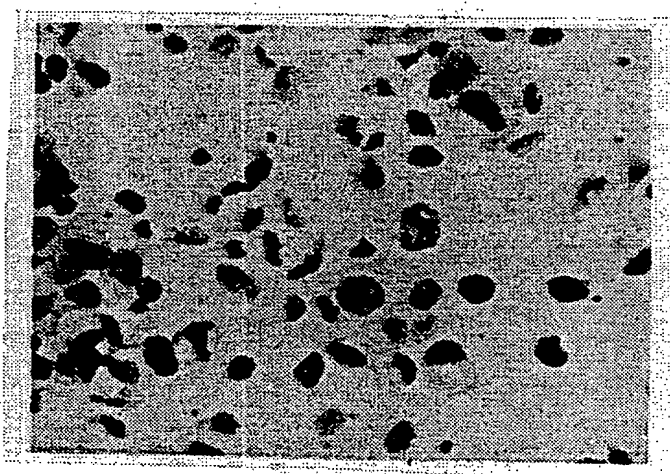
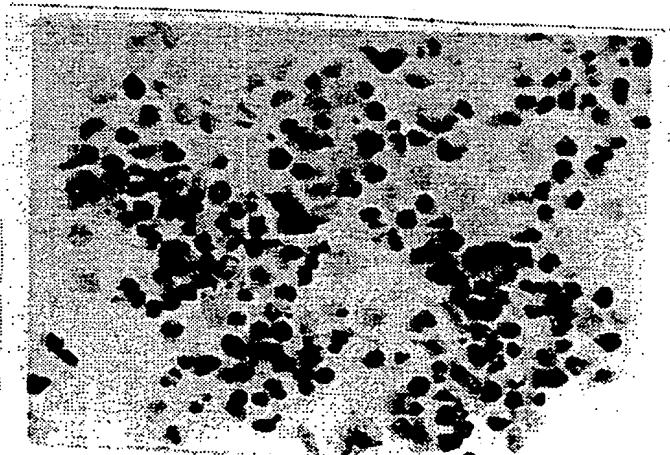
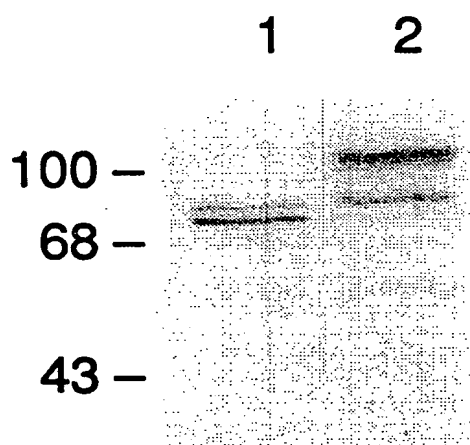


FIGURE 17C



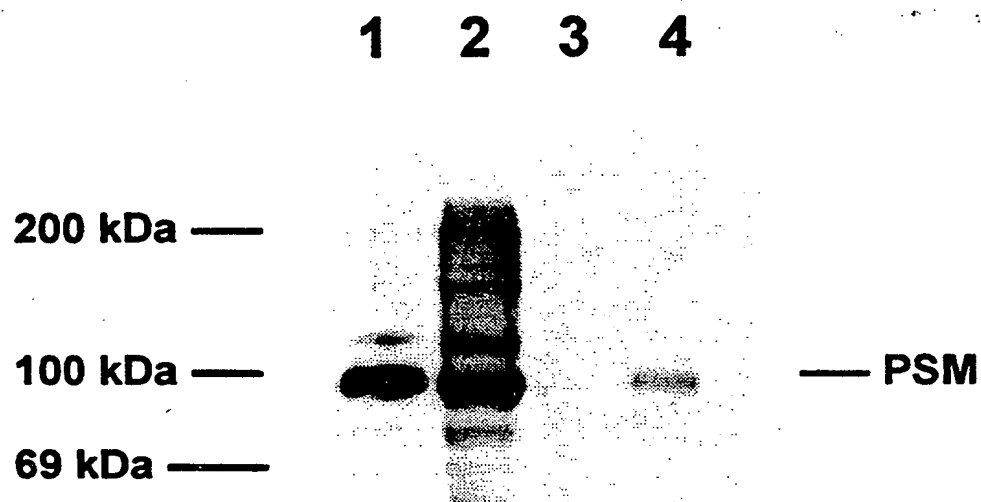
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FIGURE 18



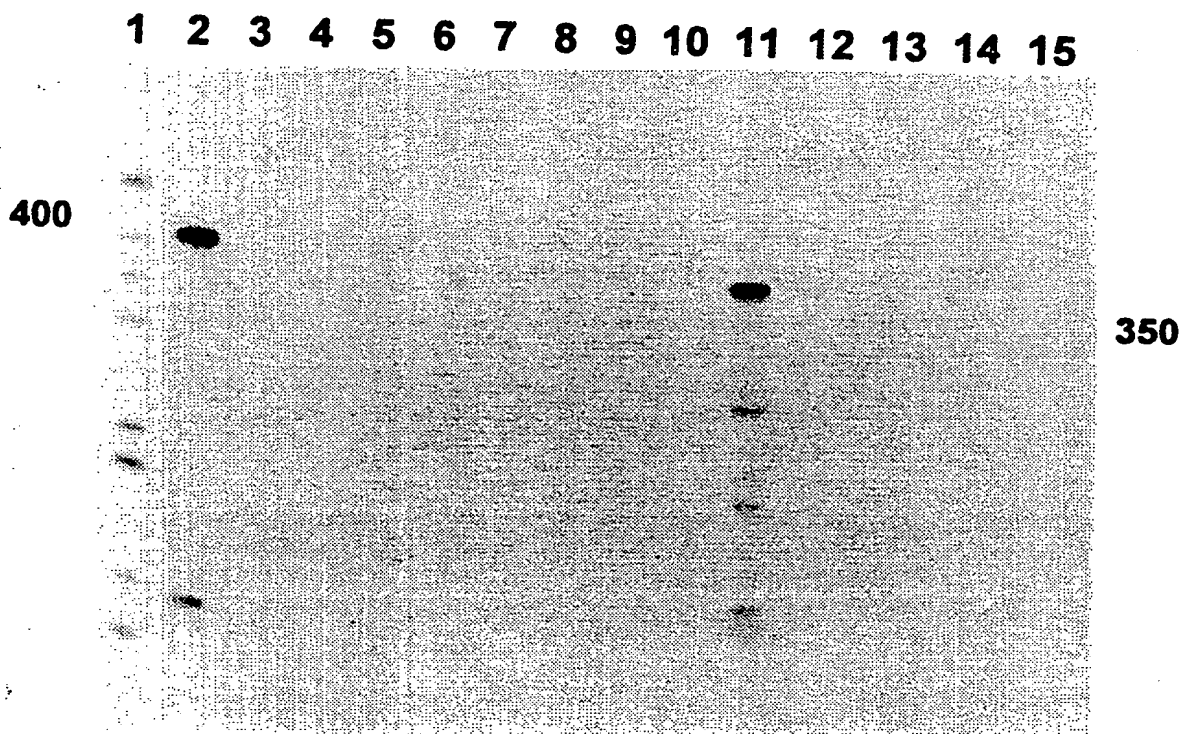
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FIGURE 19



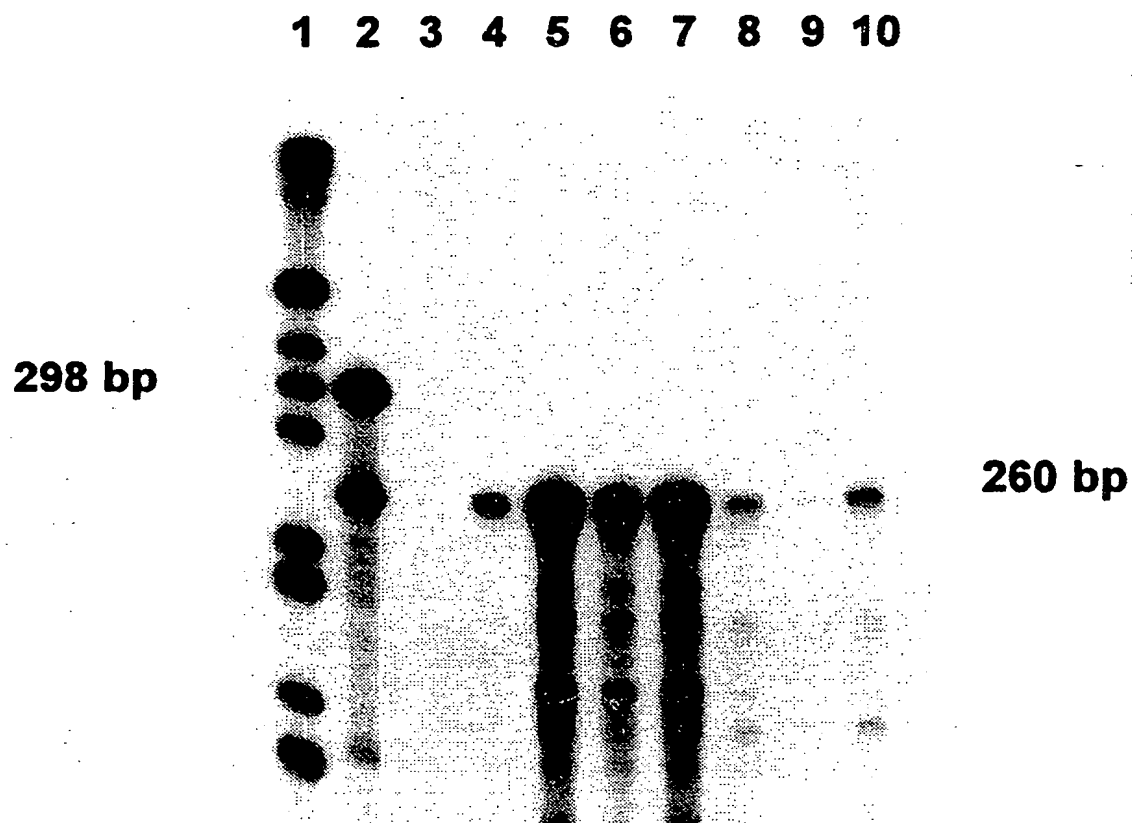
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FIGURE 20



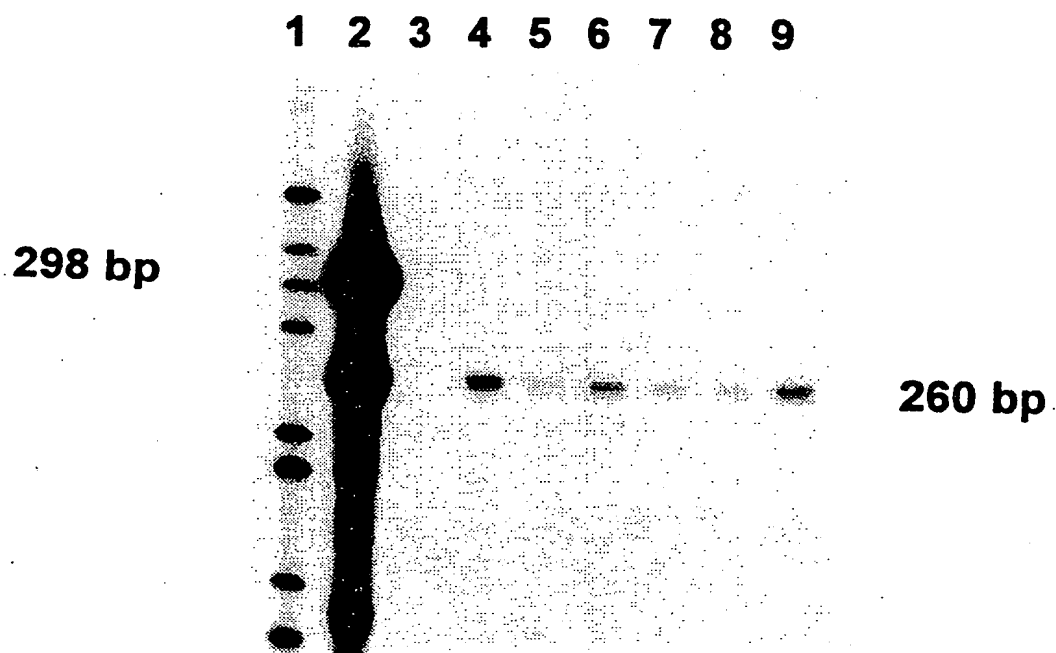
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FIGURE 21



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FIGURE 22



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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

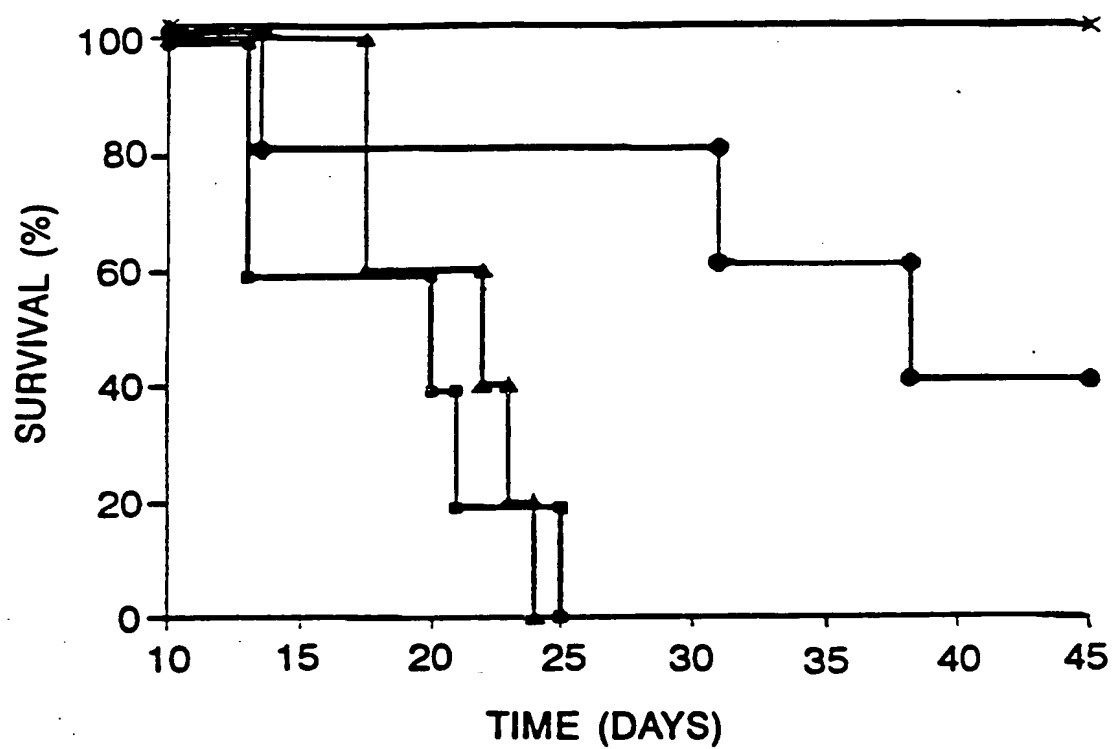
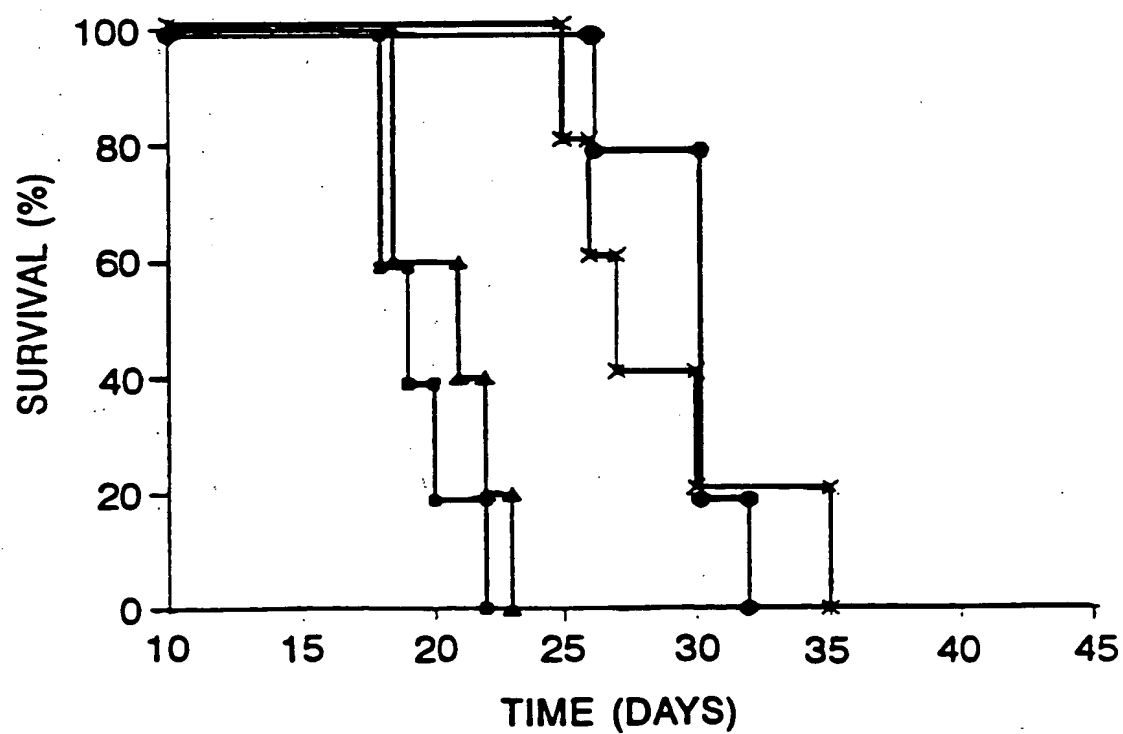


FIGURE 24B



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FIGURE 25A

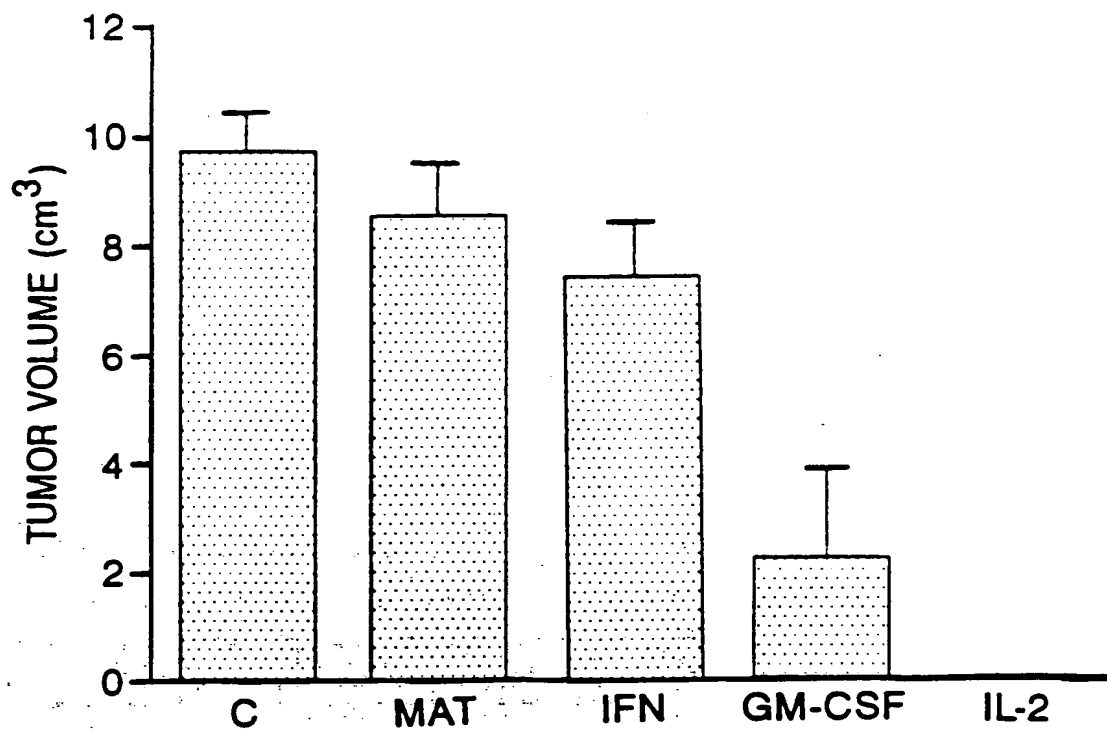
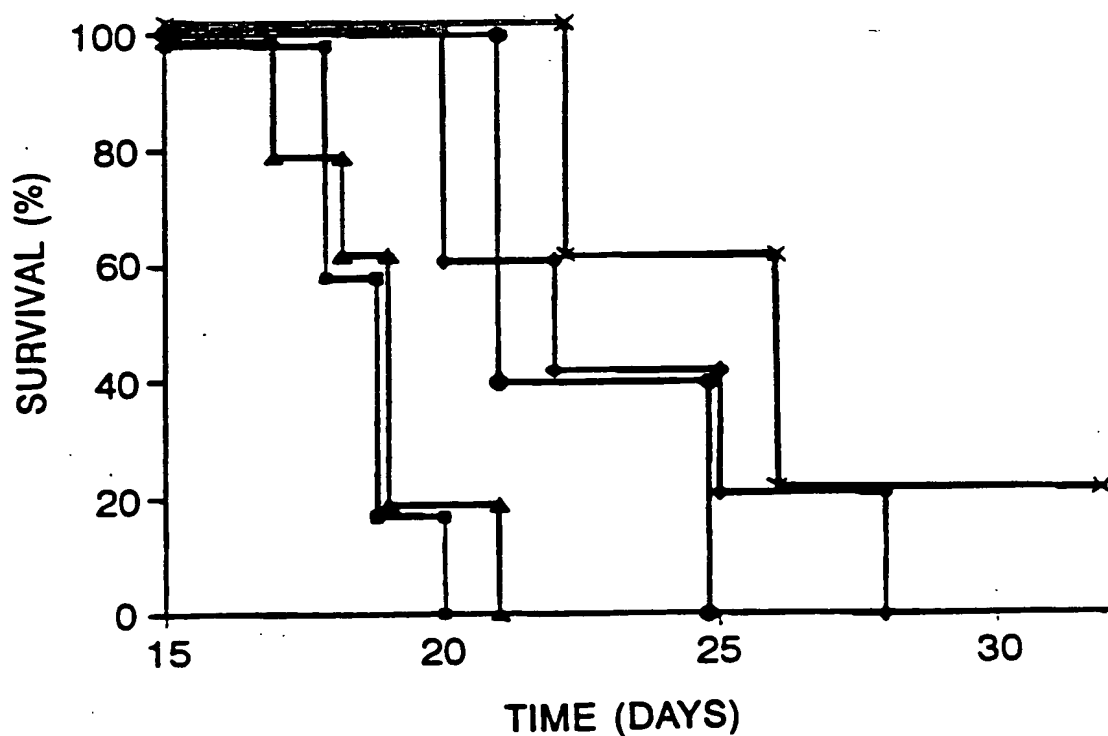
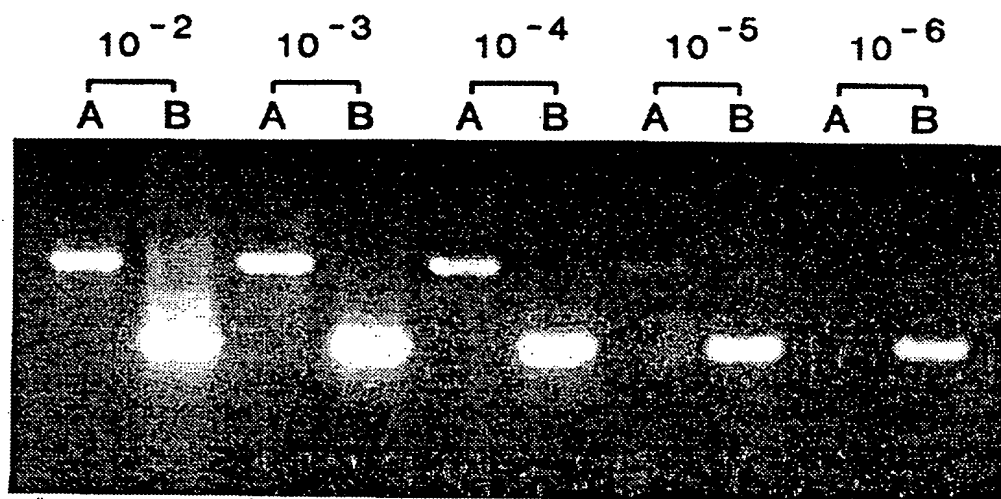


FIGURE 25B



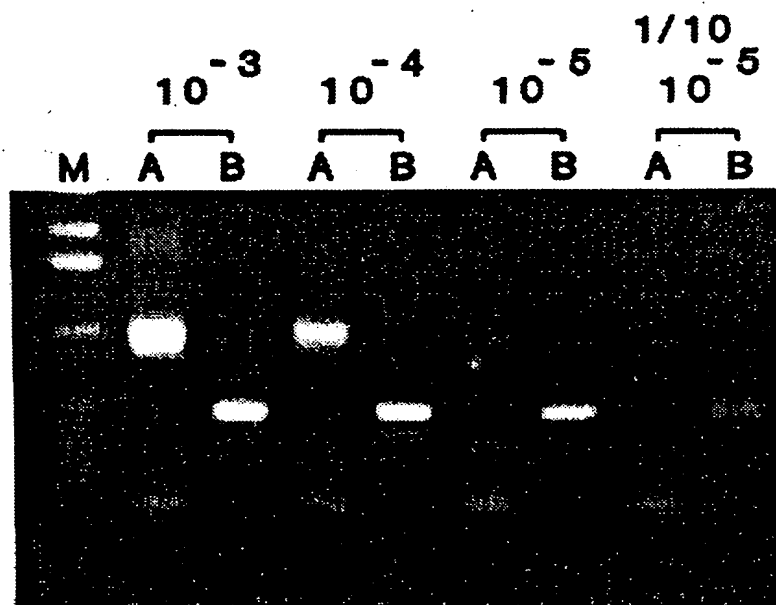
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FIGURE 26



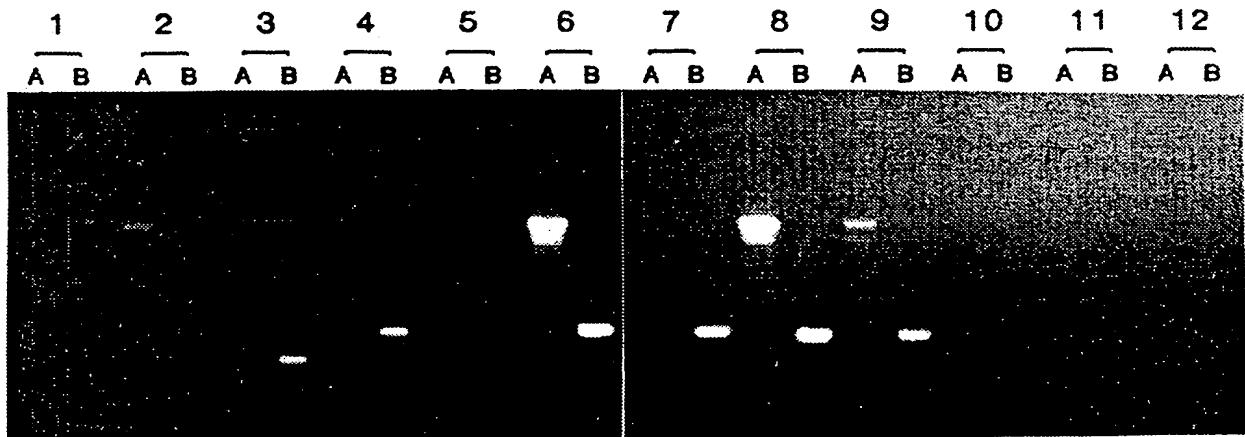
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FIGURE 27



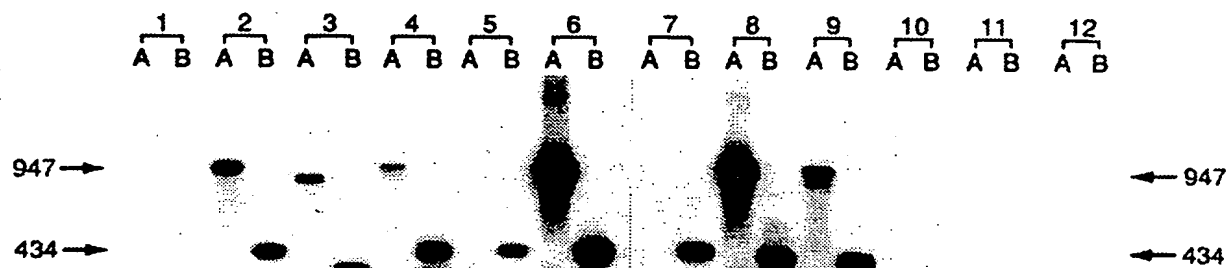
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-